## SEQUENCE LISTING

(1)   GENERAL INFORMATION:

   (i)   APPLICANT:

      (A)   NAME: RHONE-POULENC RORER S.A.

5       (B)   STREET: 20, avenue Raymond ARON

      (C)   CITY: ANTONY

      (E)   COUNTRY: FRANCE

      (F)   POSTAL CODE: 92165

   (ii)   TITLE OF INVENTION: NOVEL TOPOISOMERASE IV,

10  CORRESPONDING NUCLEOTIDE SEQUENCES AND USES.

   (iii)   NUMBER OF SEQUENCES: 14

   (iv)   COMPUTER READABLE FORM:

      (A)   MEDIUM TYPE: tape

      (B)   COMPUTER: IBM PC compatible

15       (C)   OPERATING SYSTEM: PC-DOS/MS-DOS

      (D)   SOFTWARE: PatentIn Release #1.0,

          Version #1.25 (EPO)

(2)   INFORMATION FOR SEQ ID NO: 1:

   (i)   SEQUENCE CHARACTERISTICS:

20       (A)   LENGTH: 4565 base pairs

      (B)   TYPE: nucl ic acid

      (C)   STRANDEDNESS: doubl

      (D)   TOPOLOGY: linear

(ii)    MOLECULE TYPE: cDNA

(iii)   HYPOTHETICAL: NO

(iii)   ANTISENSE: NO

(vi)    ORIGINAL SOURCE:

5               (A) ORGANISM: Staphylococcus aureus

(xi)    SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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        10         20         30         40         50         60
GAATTCCGAC GTACGTTTGC AGGAGGCGAA ATCATTGGCA ATGAATAAAC AAAATAATTA
CTTAAGGCTG CATGCAAACG TCCTCCGCTT TAGTAACCGT TACTTATTTG TTTTATTAAT

        70         80         90        100        110        120
TTCAGATGAT TCAATACAGG TTTTAGAGGG GTTAGAAGCA GTTCGTAAAA GACCTGGTAT
AAGTCTACTA AGTTATGTCC AAAATCTCCC CAATCTTCGT CAAGCATTTT CTGGACCATA

       130        140        150        160        170        180
GTATATTGGA TCAACTGATA AACGGGGATT ACATCATCTA GTATATGAAA TTGTCGATAA
CATATAACCT AGTTGACTAT TTGCCCCTAA TGTAGTAGAT CATATACTTT AACAGCTATT
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          190       200       210       220       230       240
CTCCGTCGAT GAAGTATTGA ATGGTTACGG TAACGAAATA GATGTAACAA TTAATAAAGA
GAGGCAGCTA CTTCATAACT TACCAATGCC ATTGCTTTAT CTACATTGTT AATTATTTCT

          250       260       270       280       290       300
TGGTAGTATT TCTATAGAAG ATAATGGACG TGGTATGCCA ACAGGTATAC ATAAATCAGG
ACCATAATAA AGATATCTTC TATTACCTGC ACCATACGGT TGTCCATATG TATTTAGTCC

          310       320       330       340       350       360
TAAACCGACA GTCGAAGTTA TCTTTACTGT TTTACATGCA GGAGGTAAAT TTGGACAAGG
ATTTGGCTGT CAGCTTCAAT AGAAATGACA AAATGTACGT CCTCCATTTA AACCTGTTCC

          370       380       390       400       410       420
TGGCTATAAA ACTTCAGGTG GTCTTCACGG CGTTGGTGCT TCAGTGGTAA ATGCATTGAG
ACCGATATTT TGAAGTCCAC CAGAAGTGCC GCAACCACGA AGTCACCATT TACGTAACTC

          430       440       450       460       470       480
TGAATGGCTT GAAGTTGAAA TCCATCGAGA TGGTAATATA TATCATCAAA GTTTTAAAAA
ACTTACCGAA CTTCAACTTT AGGTAGCTCT ACCATTATAT ATAGTAGTTT CAAAATTTTT

          490       500       510       520       530       540
CGGTGGTTCG CCATCTTCAG GTTTAGTGAA AAAAGGTAAA ACTAAGAAAA CAGGTACCAA
GCCACCAAGC GGTAGAAGTC CAAATCACTT TTTTCCATTT TGATTCTTTT GTCCATGGTT

          550       560       570       580       590       600
AGTAACATTT AAACCTGATG ACACAATTTT TAAAGCATCT ACATCATTTA ATTTTGATGT
TCATTGTAAA TTTGGACTAC TGTGTTAAAA ATTTCGTAGA TGTAGTAAAT TAAAACTACA

          610       620       630       640       650       660
TTTAAGTGAA CGACTACAAG AGTCTGCGTT CTTATTGAAA AATTTAAAAA TAACGCTTAA
AAATTCACTT GCTGATGTTC TCAGACGCAA GAATAACTTT TTAAATTTTT ATTGCGAATT

          670       680       690       700       710       720
TGATTTACGC AGTGGTAAAG AGCGTCAAGA GCATTACCAT TATGAAGAAG GAATCAAAGA
ACTAAATGCG TCACCATTTC TCGCAGTTCT CGTAATGGTA ATACTTCTTC CTTAGTTTCT

          730       740       750       760       770       780
GTTTGTTAGT TATGTCAATG AAGGAAAAGA AGTTTTGCAT GACGTGGCTA CATTTTCAGG
CAAACAATCA ATACAGTTAC TTCCTTTTCT TCAAAACGTA CTGCACCGAT GTAAAAGTCC

          790       800       810       820       830       840
TGAAGCAAAT GGTATAGAGG TAGACGTAGC TTTCCAATAT AATGATCAAT ATTCAGAAAG
ACTTCGTTTA CCATATCTCC ATCTGCATCG AAAGGTTATA TTACTAGTTA TAAGTCTTTC

          850       860       870       880       890       900
TATTTTAAGT TTTGTAAATA ATGTACGTAC TAAAGATGGT GGTACACATG AAGTTGGTTT
ATAAAATTCA AAACATTTAT TACATGCATG ATTTCTACCA CCATGTGTAC TTCAACCAAA

          910       920       930       940       950       960
TAAAACAGCA ATGACACGCG TATTTAATGA TTATGCACGT CGTATTAATG AACTTAAAAC
ATTTTGTCGT TACTGTGCGC ATAAATTACT AATACGTGCA GCATAATTAC TTGAATTTTG

          970       980       990       1000      1010      1020
AAAAGATAAA AACTTAGATG GTAATGATAT TCGTGAAGGT TTAACAGCTG TTGTGTCTGT
TTTTCTATTT TTGAATCTAC CATTACTATA AGCACTTCCA AATTGTCGAC AACACAGACA

          1030      1040      1050      1060      1070      1080
TCGTATTCCA GAAGAATTAT TGCAATTTGA AGGACAAACG AAATCTAAAT TGGGTACTTC
AGCATAAGGT CTTCTTAATA ACGTTAAACT TCCTGTTTGC TTTAGATTTA ACCCATGAAG
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          1090       1100       1110       1120       1130       1140
      TGAAGCTAGA AGTGCTGTTG ATTCAGTTGT TGCAGACAAA TTGCCATTCT ATTTAGAAGA
      ACTTCGATCT TCACGACAAC TAAGTCAACA ACGTCTGTTT AACGGTAAGA TAAATCTTCT

          1150       1160       1170       1180       1190       1200
      AAAAGGACAA TTGTCTAAAT CACTTGTGAA AAAAGCGATT AAAGCACAAC AAGCAAGGGA
      TTTTCCTGTT AACAGATTTA GTGAACACTT TTTTCGCTAA TTTCGTGTTG TTCGTTCCCT

          1210       1220       1230       1240       1250       1260
      AGCTGCACGT AAAGCTCGTG AAGATGCTCG TTCAGGTAAG AAAAAGAAGC GTAAAGACAC
      TCGACGTGCA TTTCGAGCAC TTCTACGAGC AAGTCCATTC TTTTGTTCG CATTTCTGTG

          1270       1280       1290       1300       1310       1320
      TTTGCTATCT GGTAAATTAA CACCTGCACA AAGTAAAAAC ACTGAAAAAA ATGAATTGTA
      AAACGATAGA CCATTTAATT GTGGACGTGT TTCATTTTTG TGACTTTTTT TACTTAACAT

          1330       1340       1350       1360       1370       1380
      TTTAGTCGAA GGTGATTCTG CGGGAGGTTC AGCAAAACTT GGACGAGACC GCAAATTCCA
      AAATCAGCTT CCACTAAGAC GCCCTCCAAG TCGTTTTGAA CCTGCTCTGG CGTTTAAGGT

          1390       1400       1410       1420       1430       1440
      AGCGATATTA CCATTACGTG GTAAGGTAAT TAATACAGAG AAAGCACGTC TAGAAGATAT
      TCGCTATAAT GGTAATGCAC CATTCCATTA ATTATGTCTC TTTCGTGCAG ATCTTCTATA

          1450       1460       1470       1480       1490       1500
      TTTTAAAAAT GAAGAAATTA ATACAATTAT CCACACAATC GGGGCAGGCG TTGGTACTGA
      AAAATTTTTA CTTCTTTAAT TATGTTAATA GGTGTGTTAG CCCCGTCCGC AACCATGACT

          1510       1520       1530       1540       1550       1560
      CTTTAAAATT GAAGATAGTA ATTATAATCG TGTAATTATT ATGACTGATG CTGATACTGA
      GAAATTTTAA CTTCTATCAT TAATATTAGC ACATTAATAA TACTGACTAC GACTATGACT

          1570       1580       1590       1600       1610       1620
      TGGTGCGCAT ATTCAAGTGC TATTGTTAAC ATTCTTCTTC AAATATATGA AACCGCTTGT
      ACCACGCGTA TAAGTTCACG ATAACAATTG TAAGAAGAAG TTTATATACT TTGGCGAACA

          1630       1640       1650       1660       1670       1680
      TCAAGCAGGT CGTGTATTTA TTGCTTTACC TCCACTTTAT AAATTGGAAA AAGGTAAAGG
      AGTTCGTCCA GCACATAAAT AACGAAATGG AGGTGAAATA TTTAACTTTT TTCCATTTCC

          1690       1700       1710       1720       1730       1740
      CAAAACAAAG CGAGTTGAAT ACGCTTGGAC AGACGAAGAG CTTAATAAAT TGCAAAAAGA
      GTTTTGTTTC GCTCAACTTA TGCGAACCTG TCTGCTTCTC GAATTATTTA ACGTTTTTCT

          1750       1760       1770       1780       1790       1800
      ACTTGGTAAA GGCTTCACGT TACAACGTTA CAAAGGTTTG GGTGAAATGA ACCCTGAACA
      TGAACCATTT CCGAAGTGCA ATGTTGCAAT GTTTCCAAAC CCACTTTACT TGGGACTTGT

          1810       1820       1830       1840       1850       1860
      ATTATGGGAA ACGACGATGA ACCCAGAAAC ACGAACTTTA ATTCGTGTAC AAGTTAAAGA
      TAATACCCTT TGCTGCTACT TGGGTCTTTG TGCTTGAAAT TAAGCACATG TTCAACTTCT

          1870       1880       1890       1900       1910       1920
      TGAAGTGCGT TCATCTAAAC GTGTAACAAC ATTAATGGGT GACAAAGTAC AACCTAGACG
      ACTTCACGCA AGTAGATTTG CACATTGTTG TAATTACCCA CTGTTTCATG TTGGATCTGC
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        1930        1940        1950        1960        1970        1980
TGAATGGATT GAAAAGCATG TTGAGTTTGG TATGCAAGAG GACCAAAGTA TTTTAGATAA
ACTTACCTAA CTTTTCGTAC AACTCAAACC ATACGTTCTC CTGGTTTCAT AAAATCTATT


        1990        2000        2010        2020        2030        2040
TTCTGAAGTA CAAGTGCTTG AAAATGATCA ATTTGATGAG GAGGAAATCT AGTGAGTGAA
AAGACTTCAT GTTCACGAAC TTTTACTAGT TAAACTACTC CTCCTTTAGA TCACTCACTT


        2050        2060        2070        2080        2090        2100
ATAATTCAAG ATTTATCACT TGAAGATGTT TTAGGTGATC GCTTTGGAAG ATATAGTAAA
TATTAAGTTC TAAATAGTGA ACTTCTACAA AATCCACTAG CGAAACCTTC TATATCATTT


        2110        2120        2130        2140        2150        2160
TATATTATTC AAGAGCGTGC ATTGCCAGAT GTTCGTGATG GTTTAAAACC AGTACAACGT
ATATAATAAG TTCTCGCACG TAACGGTCTA CAAGCACTAC CAAATTTTGG TCATGTTGCA


        2170        2180        2190        2200        2210        2220
CGTATTTTAT ACGCAATGTA TTCAAGTGGT AATACACACG ATAAAAATTT CCGTAAAAGT
GCATAAAATA TGCGTTACAT AAGTTCACCA TTATGTGTGC TATTTTTAAA GGCATTTTCA


        2230        2240        2250        2260        2270        2280
GCGAAAACAG TCGGTGATGT TATTGGTCAA TATCATCCAC ATGGAGACTC CTCAGTGTAC
CGCTTTTGTC AGCCACTACA ATAACCAGTT ATAGTAGGTG TACCTCTGAG GAGTCACATG


        2290        2300        2310        2320        2330        2340
GAAGCAATGG TCCGTTTAAG TCAAGACTGG AAGTTACGAC ATGTCTTAAT AGAAATGCAT
CTTCGTTACC AGGCAAATTC AGTTCTGACC TTCAATGCTG TACAGAATTA TCTTTACGTA


        2350        2360        2370        2380        2390        2400
GGTAATAATG GTAGTATCGA TAATGATCCG CCAGCGGCAA TGCCGTTACAC TGAAGCTAAG
CCATTATTAC CATCATAGCT ATTACTAGGC GGTCGCCGTT ACGCAATGTG ACTTCGATTC


        2410        2420        2430        2440        2450        2460
TTAAGCTTAC TAGCTGAAGA GTTATTACGT GATATTAATA AAGAGACAGT TTCTTTCATT
AATTCGAATG ATCGACTTCT CAATAATGCA CTATAATTAT TTCTCTGTCA AAGAAAGTAA


        2470        2480        2490        2500        2510        2520
CCAAACTATG ATGATACGAC ACTCGAACCA ATGGTATTGC CATCAAGATT TCCTAACTTA
GGTTTGATAC TACTATGCTG TGAGCTTGGT TACCATAACG GTAGTTCTAA AGGATTGAAT


        2530        2540        2550        2560        2570        2580
CTAGTGAATG GTTCTACAGG TATATCTGCA GGTTACGCGA CAGATATACC ACCACATAAT
GATCACTTAC CAAGATGTCC ATATAGACGT CCAATGCGCT GTCTATATGG TGGTGTATTA


        2590        2600        2610        2620        2630        2640
TTAGCTGAAG TGATTCAAGC AACACTTAAA TATATTGATA ATCCGGATAT TACAGTCAAT
AATCGACTTC ACTAAGTTCG TTGTGAATTT ATATAACTAT TAGGCCTATA ATGTCAGTTA


        2650        2660        2670        2680        2690        2700
CAATTAATGA AATATATTAA AGGTCCTGAT TTTCCAACTG GTGGTATTAT TCAAGGTATT
GTTAATTACT TTATATAATT TCCAGGACTA AAAGGTTGAC CACCATAATA AGTTCCATAA


        2710        2720        2730        2740        2750        2760
GATGGTATTA AAAAAGCTTA TGAATCAGGT AAAGGTAGAA TTATAGTTCG TTCTAAAGTT
CTACCATAAT TTTTTCGAAT ACTTAGTCCA TTTCCATCTT AATATCAAGC AAGATTTCAA


        2770        2780        2790        2800        2810        2820
GAAGAAGAAA CTTTACGCAA TGGACGTAAA CAGTTAATTA TTACTGAAAT TCCATATGAA
CTTCTTCTTT GAAATGCGTT ACCTGCATTT GTCAATTAAT AATGACTTTA AGGTATACTT
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        2830       2840       2850       2860       2870       2880
GTGAACAAAG GTAGCTTAGT AAAACGTATC GATGAATTAC GTGCTGACAA AAAAGTCGAT
CACTTGTTTC CATCGAATCA TTTTGCATAG CTACTTAATG CACGACTGTT TTTTCAGCTA

        2890       2900       2910       2920       2930       2940
GGTATCGTTG AAGTACGTGA TGAAACTGAT AGAACTGGTT TACGAATAGC AATTGAATTG
CCATAGCAAC TTCATGCACT ACTTTGACTA TCTTGACCAA ATGCTTATCG TTAACTTAAC

        2950       2960       2970       2980       2990       3000
AAAAAAGATG TGAACAGTGA ATCAATCAAA AATTATCTTT ATAAAAACTC TGATTTACAG
TTTTTTCTAC ACTTGTCACT TAGTTAGTTT TTAATAGAAA TATTTTTGAG ACTAAATGTC

        3010       3020       3030       3040       3050       3060
ATTTCATATA ATTTCAACAT GGTCGCTATT AGTGATGGTC GTCCAAAATT GATGGGTATT
TAAAGTATAT TAAAGTTGTA CCAGCGATAA TCACTACCAG CAGGTTTTAA CTACCCATAA

        3070       3080       3090       3100       3110       3120
CGTCAAATTA TAGATAGTTA TTTGAATCAT CAAATTGAGG TTGTTGCAAA TAGAACGAAG
GCAGTTTAAT ATCTATCAAT AAACTTAGTA GTTTAACTCC AACAACGTTT ATCTTGCTTC

        3130       3140       3150       3160       3170       3180
TTTGAATTAG ATAATGCTGA AAAACGTATG CATATCGTTG AAGGTTTGAT TAAAGCGTTG
AAACTTAATC TATTACGACT TTTTGCATAC GTATAGCAAC TTCCAAACTA ATTTCGCAAC

        3190       3200       3210       3220       3230       3240
TCAATTTTAG ATAAAGTAAT CGAATTGATT CGTAGCTCTA AAAACAAGCG TGACGCTAAA
AGTTAAAATC TATTTCATTA GCTTAACTAA GCATCGAGAT TTTTGTTCGC ACTGCGATTT

        3250       3260       3270       3280       3290       3300
GAAAACCTTA TCGAAGTATA CGAGTTCACA GAAGAACAGG CTGAAGCAAT TGTAATGTTA
CTTTTGGAAT AGCTTCATAT GCTCAAGTGT CTTCTTGTCC GACTTCGTTA ACATTACAAT

        3310       3320       3330       3340       3350       3360
CAGTTATATC GTTTAACAAA CACTGACATA GTTGCGCTTG AAGGTGAACA TAAAGAACTT
GTCAATATAG CAAATTGTTT GTGACTGTAT CAACGCGAAC TTCCACTTGT ATTTCTTGAA

        3370       3380       3390       3400       3410       3420
GAAGCATTAA TCAAACAATT ACGTCATATT CTTGATAACC ATGATGCATT ATTGAATGTC
CTTCGTAATT AGTTTGTTAA TGCAGTATAA GAACTATTGG TACTACGTAA TAACTTACAG

        3430       3440       3450       3460       3470       3480
ATAAAAGAAG AATTGAATGA AATTAAAAAG AAATTCAAAT CTGAACGACT GTCTTTAATT
TATTTTCTTC TTAACTTACT TTAATTTTTC TTTAAGTTTA GACTTGCTGA CAGAAATTAA

        3490       3500       3510       3520       3530       3540
GAAGCAGAAA TTGAAGAAAT TAAAATTGAC AAAGAAGTTA TGGTGCCTAG TGAAGAAGTT
CTTCGTCTTT AACTTCTTTA ATTTTAACTG TTTCTTCAAT ACCACGGATC ACTTCTTCAA

        3550       3560       3570       3580       3590       3600
ATTTTAAGTA TGACACGTCA TGGATATATT AAACGTACTT CTATTCGTAG CTTTAATGCT
TAAAATTCAT ACTGTGCAGT ACCTATATAA TTTGCATGAA GATAAGCATC GAAATTACGA

        3610       3620       3630       3640       3650       3660
AGCGGTGTTG AAGATATTGG TTTAAAAGAT GGTGACAGTT TACTTAAACA TCAAGAAGTA
TCGCCACAAC TTCTATAACC AAATTTTCTA CCACTGTCAA ATGAATTTGT AGTTCTTCAT
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        3670        3680        3690        3700        3710        3720
AATACGCAAG ATACCGTACT AGTATTTACA AATAAAGGTC GTTATCTATT TATACCAGTT
TTATGCGTTC TATGGCATGA TCATAAATGT TTATTTCCAG CAATAGATAA ATATGGTCAA

        3730        3740        3750        3760        3770        3780
CATAAATTAC GAGATATTCG TTGGAAAGAA TTGGGGCAAC ATGTATCACA AATAGTTCCT
GTATTTAATG CTCTATAAGC AACCTTTCTT AACCCCGTTG TACATAGTGT TTATCAAGGA

        3790        3800        3810        3820        3830        3840
ATCGAAGAAG ATGAAGTGGT TATTAATGTC TATAATGAAA AGGACTTTAA TACTGATGCA
TAGCTTCTTC TACTTCACCA ATAATTACAG ATATTACTTT TCCTGAAATT ATGACTACGT

        3850        3860        3870        3880        3890        3900
TTTTATGTTT TTGCGACTCA AAATGGCATG ATTAAGAAAA GTACAGTGCC TCTATTTAAA
AAAATACAAA AACGCTGAGT TTTACCGTAC TAATTCTTTT CATGTCACGG AGATAAATTT

        3910        3920        3930        3940        3950        3960
ACAACGCGTT TTAATAAACC TTTAATTGCA ACTAAAGTTA AAGAAAATGA TGATTTGATT
TGTTGCGCAA AATTATTTGG AAATTAACGT TGATTTCAAT TTCTTTTACT ACTAAACTAA

        3970        3980        3990        4000        4010        4020
AGTGTTATGC GCTTTGAAAA AGATCAATTA ATTACCGTAA TTACAAATAA AGGTATGTCA
TCACAATACG CGAAACTTTT TCTAGTTAAT TAATGGCATT AATGTTTATT TCCATACAGT

        4030        4040        4050        4060        4070        4080
TTAACGTATA ATACAAGTGA ACTATCAGAT ACTGGATTAA GGGCGGCTGG TGTTAAATCA
AATTGCATAT TATGTTCACT TGATAGTCTA TGACCTAATT CCCGCCGACC ACAATTTAGT

        4090        4100        4110        4120        4130        4140
ATAAATCTTA AAGTTGAAGA TTTCGTTGTT ATGACAGAAG GTGTTTCTGA AAATGATACT
TATTTAGAAT TTCAACTTCT AAAGCAACAA TACTGTCTTC CACAAAGACT TTTACTATGA

        4150        4160        4170        4180        4190        4200
ATATTGATGG CCACACAACG CGGCTCGTTA AAACGTATTA GTTTTAAAAT CTTACAAGTT
TATAACTACC GGTGTGTTGC GCCGAGCAAT TTTGCATAAT CAAAATTTTA GAATGTTCAA

        4210        4220        4230        4240        4250        4260
GCTAAAAGAG CACAACGTGG AATAACTTTA TTAAAAGAAT TAAAGAAAAA TCCACATCGT
CGATTTTCTC GTGTTGCACC TTATTGAAAT AATTTTCTTA ATTTCTTTTT AGGTGTAGCA

        4270        4280        4290        4300        4310        4320
ATAGTAGCTG CACATGTAGT GACAGGTGAA CATAGTCAAT ATACATTATA TTCAAAATCA
TATCATCGAC GTGTACATCA CTGTCCACTT GTATCAGTTA TATGTAATAT AAGTTTTAGT

        4330        4340        4350        4360        4370        4380
AACGAAGAAC ATGGTTTAAT TAATGATATT CATAAATCTG AACAATATAC AAATGGCTCA
TTGCTTCTTG TACCAAATTA ATTACTATAA GTATTTAGAC TTGTTATATG TTTACCGAGT

        4390        4400        4410        4420        4430        4440
TTCATTGTAG ATACAGATGA TTTTGGTGAA GTAATAGACA TGTATATTAG CTAAAAACTA
AAGTAACATC TATGTCTACT AAAACCACTT CATTATCTGT ACATATAATC GATTTTTGAT

        4450        4460        4470        4480        4490        4500
TATGCAATCA CGAAATTAAA TGATAAAATA CAGTAATGTT AAATTTTGAC TAAATTCAAG
ATACGTTAGT GCTTTAATTT ACTATTTTAT GTCATTACAA TTTAAAACTG ATTTAAGTTC
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        4510       4520       4530    ·    4540       4550       4560
GGATTTATAT TAAATGCTGA CCAAGTACTT ATCGT.AAAT TAGCGATACG GAATCCGCGG
CCTAAATATA ATTTACGACT GGTTCATGAA TAGCAATTTA ATCGCTATGC CTTAGGCGCC


AATTC
TTAAG
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(3)   INFORMATION FOR SEQ ID NO: 2:


    (i)     SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 2402 base pairs

            (B)   TYPE: nucleic acid

            (C)   STRANDEDNESS: single

            (D)   TOPOLOGY: linear


    (ii)    MOLECULE TYPE: cDNA


    (iii)   HYPOTHETICAL: NO


    (iii)   ANTISENSE: NO


    (vi)    ORIGINAL SOURCE:

            (A) ORGANISM: Staphylococcus aureus


    (xi)    SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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        M  S  E  I  I  C  D  L  S  L  E  D  V  L  G  D  R  F  G  R  Y  S  K  Y  I
        GTGAGTGAAATAATTCAAGATTTATCACTTGAAGATGTTTTAGGTGATCGCTTTGGAAGATATAGTAAATATATT
        2032      2042      2052      2062      2072      2082      2092      2102


        I  Q  E  R  A  L  P  D  V  R  D  G  L  K  P  V  Q  R  R  I  L  Y  A  M  Y
        ATTCAAGAGCGTGCATTGCCAGATGTTCGTGATGGTTTAAAACCAGTACAACGTCGTATTTTATACGCAATGTAT
        2107      2117      2127      2137      2147      2157      2167      2177


        S  S  G  N  T  H  D  K  N  F  R  K  S  A  K  T  V  G  D  V  I  G  Q  Y  H
        TCAAGTGGTAATACACACGATAAAAATTTCCGTAAAAGTGCGAAAACAGTCGGTGATGTTATTGGTCAACATCAT
        2182      2192      2202      2212      2222      2232      2242      2252


        F  H  G  C  S  S  V  Y  E  A  M  V  R  L  S  Q  D  W  K  L  R  H  V  L  I
        CCACATGGAGACTCCTCAGTGTACGAAGCAATGGTCCGTTTAAGTCAAGACTGGAAGTTACGACATGTCTTAATA
        2257      2267      2277      2287      2297      2307      2317      2327


        E  M  H  G  N  N  G  S  I  D  N  D  P  P  A  A  M  R  Y  T  E  A  K  L  S
        GAAATGCATGGTAATAATGGTAGTATCGATAATGATCCGCCAGCGGCAATGCGTTACACTGAAGCTAAGTTAAGC
        2332      2342      2352      2362      2372      2382      2392      2402


        L  L  A  E  E  L  L  R  D  I  N  K  E  T  V  S  F  I  P  N  Y  D  D  T  T
        TTACTAGCTGAAGAGTTATTACGTGATATTAATAAAGAGACAGTTTCTTTCATTCCAAACTATGATGATACGACA
        2407      2417        2427      2437      2447      2457      2467      2477


        L  E  F  H  V  L  F  S  R  F  F  R  L  L  V  H  S  S  T  G  I  S  A  G  Y
        CTCGAACCAGTGGTATTGCCATCAAGATTTCCTAACTTACTAGTGAATGGTTCTACAGGTATATCTGCAGGTTAC
        2482      2492      2502      2512      2522      2532      2542      2552


        A  T  C  I  F  F  H  N  L  A  E  V  I  Q  A  T  L  M  Y  I  D  N  P  D  I
        GCGACAGATATACCACCACATAATTTAGCTGAAGTGATTCAAGCAACACTTAAATATATTGATAATCCGGATATT
        2557      2567      2577      2587      2597      2607      2617      2627
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          T  V  R   L  M  F  Y  I  K  S  F  F  F  F  T  S  S  I  I  U  G  I  D  G
       ACAGTCAATCAATTAATGAAATATATTAAAGGTCCTGATTTTCCAACTSGTGGTATTATTCAAGGTATTGATGGT
      2631      2641      2651      2661      2671      2681      2691      2701

          I  K  K  A  Y  E  S  G  K  G  R  I  I  V  R  E  K  V  E  E  E  T  L  R  N
       ATTAAAAAGGCTTATGAATCAGGTAAAGGTAGAATTATAGTTCGTTCTAAAGTTGAAGAAGAAACTTTACGCAAT
      2707      2717      2727      2737      2747      2757      2767      2777

          G  R  K  Q  L  I  I  T  E  I  P  Y  E  V  N  K  S  S  L  V  K  R  I  D  E
       GGACGTAAACAGTTAATTATTACTGAAATTCCATATGAAGTCAACAAASGTAGTTAGTAAAACGTATCGATGAA
      2782      2792      2802      2812      2822      2832      2842      2852

          L  R  A  D  K  K  V  D  G  I  V  E  V  R  D  E  T  D  R  T  G  L  R  I  A
       TTACGTGCTGACAAAAAAGTCGATGGTATCGTTGAAGTACGTGATGAAACTGATAGAACTGGTTTACGAATAGCA
      2857      2867      2877      2887      2897      2907      2917      2927

          I  E  L  K  K  D  V  N  S  E  S  I  K  N  Y  L  Y  K  N  S  D  L  Q  I  S
       ATTGAATTGAAAAAAGATGTGAACAGTGAATCAATCAAAAATTATCTTTATAAAAACTCTGATTTACAGATTTCA
      2932      2942      2952      2962      2972      2982      2992      3002

          Y  N  F  N  M  V  A  I  L  S  D  G  R  P  K  L  M  G  I  R  Q  I  I  D  S  Y
       TATAATTTCAACATGGTCGTTATTAGTGATGGTCGTCCAAAATTGATGGGTATTCGTCAAATTATAGATAGTTAT
      3007      3017      3027      3037      3047      3057      3067      3077

          L  N  H  Q  I  E  V  V  A  N  R  T  K  F  E  L  D  N  A  E  K  R  M  H  I
       TTGAATCATCAAATTGAGGTTGTTGCAAATAGAACGAAGTTTGAATTAGATAATGCTGAAAAACGTATGCATATC
      3082      3092      3102      3112      3122      3132      3142      3152

          V  E  G  L  I  K  A  L  S  I  L  D  K  V  I  E  L  I  R  S  S  K  N  K  R
       GTTGAAGGTTTGATTAAAGCGTTGTCAATTTTAGATAAAGTAATCGAATTGATTCGTAGCTCTAAAAACAAGCGT
      3157      3167      3177      3187      3197      3207      3217      3227

          D  A  K  E  N  L  I  E  V  Y  Y  E  F  T  E  E  Q  A  E  A  I  V  H  L  Q  L
       GACGCTAAAGAAAACCTTATCGAAGTATACGAGTTCACAGAAGAACAGGCTGAAGCAATTGTAATGTTACAGTTA
      3232      3242      3252      3262      3272      3282      3292      3302

          Y  R  L  T  N  T  D  I  V  A  L  E  G  E  N  K  E  L  E  A  L  I  K  Q  L
       TATCGTTTAACAAACACTGACATAGTTGCGCTTGAAGGTGAACATAAAGAACTTGAAGCATTAATCAAACAATTA
      3307      3317      3327      3337      3347      3357      3367      3377

          R  H  I  L  D  N  H  D  A  L  L  N  V  I  K  E  E  L  N  E  I  K  K  K  F
       CGTCATATTCTTGATAACCATGATGCATTATTGAATGTCATAAAAGAAGAATTGAATGAAATTAAAAAGAAATTC
      3382      3392      3402      3412      3422      3432      3442      3452

          K  S  E  R  L  S  L  I  E  A  E  I  E  E  I  K  I  D  K  E  V  M  V  P  S
       AAATCTGAACGACTGTCTTTAATTGAAGCAGAAATTGAAGAAATTAAAATTGACAAAGAAGTTATGGTGCCTAGT
      3457      3467      3477      3487      3497      3507      3517      3527

          E  E  V  I  L  S  M  T  R  H  G  Y  I  K  R  T  S  I  R  S  F  N  A  S  G
       GAAGAAGTTATTTTAAGTATGACACGTCATGGATATATTAAACGTACTTCTATTCGTAGCTTTAATGCTAGCGGT
      3532      3542      3552      3562      3572      3582      3592      3602

          V  E  D  I  G  L  K  D  G  D  S  L  L  K  H  Q  E  V  N  T  Q  D  T  V  L
       GTTGAAGATATTGGTTTAAAAGATGGTGACAGTTTACTTAAACATCAAGAAGTAAATACGCAAGATACCGTACTA
      3607      3617      3627      3637      3647      3657      3667      3677

          V  F  T  N  K  G  R  Y  L  F  I  F  V  H  K  L  R  D  I  R  W  K  E  L  G
       GTATTTACAAATAAAGGTCGTTATCTATTTATACCAGTTCATAAATTACGAGATATTCGTTGGAAAGAATTGGGG
      3682      3692      3702      3712      3722      3732      3742      3752

          Q  H  V  S  Q  I  V  F  I  E  E  D  E  V  V  I  N  V  Y  N  E  K  D  F  N
       CAACATGTATCACAAATAGTTCCTATCGAAGAAGATGAAGTGGTTATTAATGTCTATAATGAAAAGGACTTTAAT
      3757      3767      3777      3787      3797      3807      3817      3827

          T  D  A  F  I  V  F  A  T  Q  N  G  M  I  K  K  S  T  V  F  L  F  K  T  T
       ACTGATGCATTTTATGTGTTTGCGACTCAAAATGGCATGATTAAGAAAAGTACAGTGGTTCTATTTAAAACAACG
      3832      3842      3852      3862      3872      3882      3892      3902

          R  F  K  N  K  F  L  A  T  K  V  K  E  N  D  E  L  I  S  V  M  R  F  E  K
       CGTTTTAATAAAAACTTTAATTGCAACTAAAGTTAAAGAAAATGATGATTTGATTAGTGTTATGCGCTTTGAAAAA
      3907      3917      3927      3937      3947      3957      3967      3977
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    D  Q  L  I  T  V  I  T  N  K  G  H  S  L  T  T  V  K  T  S  E  L  S  D  T  G
   GATCAATTAATTACCGTAATTACAAATAAAGGTATGTCATTAACGTATAATACAAGTGAACTATCAGATACTGGA
  398:      399:      400:      4012      40::      4:3:      4042      405:

    L  R  A  A  G  V  K  S  I  N  L  K  V  E  D  T  V  V  M  T  E  G  V  S  E
   TTAAGGGCGGCTGGTGTTAAATCAATAAATCTTAAAGTTGAAGATTTCGTTGTTATGACAGAAGGTGTTTCTGAA
  405:      4067      4077:      4087      40·9:     4::·:      4::7      4127

    N  D  T  I  L  M  A  T  Q  R  G  S  L  K  K  I  S  F  K  I  L  Q  V  A  K
   AATGATACTATATTGATGGCCACACAACGCGGTCGTTAAAACGTATTAGTTTTTAAAATCTTACAAGTTGCTAAA
  4132      414:      4152      4162      417:      418:      4192      4202

    R  A  Q  R  G  I  T  L  L  L  K  E  L  K  K  N  F  H  R  I  V  A  A  H  V  V
   AGAGCACAACGTGGAATAACTTTATTAAAAGAATTAAAGAAAAATCCACATCGTATAGTAGCTGCACATGTAGTG
  4207      4217      4227      4237      4247      425:      4267      4277

    T  G  E  H  S  Q  Y  T  L  Y  S  K  S  N  E  E  H  G  L  I  N  D  L  H  K
   ACAGGTGAACATAGTCAATATACATTATATTCAAAATCAAACGAAGAACATGGTTTAATTAATGATATTCATAAA
  428:      429:      4302      431:      43::      433:      4342      435:

    S  E  Q  Y  T  N  G  S  F  I  V  D  T  D  D  F  G  E  V  I  D  N  Y  I  S
   TCTGAACAATATACAAATGGCTCATTCATTGTAGATACAGATGATTTTGGTGAAGTAATAGACATGTATATTAGC
  4357      4367      4377      4387      4397      ::·:·    ··  4417      442·

  ...
  TAA
  443::
```

(4)  INFORMATION FOR SEQ ID NO: 3:

    (i)    SEQUENCE CHARACTERISTICS:

           (A)  LENGTH: 1991 base pairs

           (B)  TYPE: nucleic acid

5          (C)  STRANDEDNESS: single

           (D)  TOPOLOGY: linear


    (ii)   MOLECULE TYPE: cDNA


    (iii)  HYPOTHETICAL: NO


    (iii)  ANTISENSE: NO


10  (vi)   ORIGINAL SOURCE:

           (A) ORGANISM: Staphylococcus aureus

(xi)　　　SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
    M N K C K N Y S D D S I G V L E G L E A V R K R F
ATGAATAAACAAAATAATTATTCAGATGATTCAATACAGGTTTTAGAGGGGTTAGAAGCAGTTCGTAAAAGACCT
41        51        61        71        81        91        101       111
    G M Y I G S T C K R G L H H L V E I V D N S V C
GGTATGTATATTGGATCAACTGATAAACGGGGATTACATCATCTAGTATATGAAATTGTCGATAACTCCGTCGAT
116       126       136       146       156       166       176       186

    E V L N G Y G N E I C V T I N H C G S I G I E D N
GAAGTATTGAATGGTTACGGTAACGAAATAGATGTAACAATTAATAAAGATGGTAGTATTTCTATAGAAGATAAT
191       201       211       221       231       241       251       261

    G R G M F T G I H K S G K F T V E V I F T V L N A
GGAGGTGGTATGCCAACAGGTATACATAAATCAGGTAAACCGACAGTCGAAGTTATCTTTACTGTTTTACATGCA
266       276       286       296       306       316       326       336
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       G   G   N   F   G   C   G   G   Y   F   T   S   G   G   L   R   G   V   G   A   F   V   V   N   A
       GGAGGTAAATTTGGACAAGGTGGCTATAAAACTTCAGGTGGTCTTCACGGCGGTTGGTGCTTCAGTGGTAAATGCA
       341       351       361       371       381       391       401       411

       L   S   E   W   L   E   V   E   I   N   K   D   G   N   I   Y   K   Q   S   F   K   N   G   G   S
       TTGAGTGAATGGCTTGAAGTTGAAATCCATCGAGATGGTAATATATATCATCAAAGTTTTAAAAACGGTGGTTCG
       416       426       436       446       456       466       476       486

       P   S   F   G   L   V   K   M   G   K   T   K   K   T   G   T   K   V   T   F   K   P   D   D   T
       CCATCTTCAGGTTTAGTGAAAAAGGTAAAACTAAGAAAACAGGTACCAAAGTAACATTTAAACCTGATGACACA
       491       501       511       521       531       541       551       561

       I   F   K   A   S   T   S   F   N   F   D   V   L   S   E   R   L   Q   E   S   A   F   L   L   K
       ATTTTTAAAGCATCTACATCATTTAATTTTGATGTTTTAAGTGAACGACTACAAGAGTCTGCCGTTCTTATTGAAA
       566       576       586       596       606       616       626       636

       N   L   K   I   T   L   N   D   L   R   S   G   K   E   R   Q   E   H   Y   H   Y   E   E   G   I
       AATTTAAAAATAACGCTTAATGATTTACGCAGTGGTAAAGAGCGTCAAGAGCATTACCATTATGAAGAAGGAATC
       641       651       661       671       681       691       701       711

       K   E   F   V   S   Y   V   N   E   G   K   E   V   L   H   D   V   A   T   F   S   G   E   A   N
       AAAGAGTTTGTTAGTTATGTCAATGAAGGAAAAGAAGTTTTGCATGACGTGGCTACATTTTCAGGTGAAGCAAAT
       716       726       736       746       756       766       776       786

       G   I   E   V   D   V   A   F   Q   Y   N   D   Q   Y   S   E   S   I   L   S   F   V   N   N   V
       GGTATAGAGGTAGACGTAGCTTTTCAATATAATGATCAATATTCAGAAAGTATTTTAAGTTTTGTAAATAATGTA
       791       801       811       821       831       841       851       861

       R   T   K   D   G   G   T   N   E   V   G   F   K   T   A   M   T   R   V   F   N   D   Y   A   R
       CGTACTAAAGATGGTGGTACAAATGAAGTTGGTTTTAAAACAGCAATGACACGCGTATTTAATGATTATGCACGT
       866       876       886       896       906       916       926       936

       R   I   N   E   L   K   T   F   D   K   N   L   D   G   N   D   I   R   E   G   L   T   A   V   V
       CGTATTAATGAATTTAAAACATTTGATAAAAACTTAGATGGTAATGATATTCGTGAAGGTTTAACAGCTGTTGTG
       941       951       961       971       981       991       1001       1011

       S   V   R   I   F   E   E   L   L   Q   F   E   G   Q   T   N   S   K   L   G   T   S   E   A   R
       TCTGTTCGTATTCCAGAAGAATTATTGCAATTTGAAGGACAAACGAAATCTAAATTGGGTACTTCTGAAGCTAGA
       1016       1026       1036       1046       1056       1066       1076       1086

       S   A   V   D   S   V   V   A   D   K   L   P   F   Y   L   E   E   K   G   Q   L   S   K   S   L
       AGTGCTGTTGATTCAGTTGTTGCAGACAAAATTGCCATTCTATTTAGAAGAAAAGGACAATTGTCTAAATCACTT
       1091       1101       1111       1121       1131       1141       1151       1161

       V   K   K   A   I   K   A   T   Q   A   R   E   A   A   R   K   A   R   E   D   A   R   S   G   K
       GTGAAAAAAGCGATTAAAGCACAACAAGCAAGGGAAGCTGCACGTAAAGCTCGTGAAGATGCTCGTTCAGGTAAG
       1166       1176       1186       1196       1206       1216       1226       1236

       K   N   E   R   F   D   T   L   L   S   G   K   L   T   P   A   Q   S   K   N   T   E   K   N   E
       AAAAACAAGCGTAAAGACACTTTGCTATCTGGTAAATTAACACCTGCACAAAGTAAAAACACTGAAAAAAATGAA
       1241       1251       1261       1271       1281       1291       1301       1311

       L   Y   L   V   E   G   D   S   A   G   G   S   A   K   L   G   R   D   R   K   F   Q   A   I   L
       TTGTATTTAGTCGAAGGTGATTCTGCGGGAGGTTCAGCAAAACTTGGACGAGACCGCAAATTCCAAGCGATATTA
       1316       1326       1336       1346       1356       1366       1376       1386

       P   L   R   G   K   V   I   N   T   E   K   A   R   L   E   D   I   F   K   N   E   E   I   N   T
       CCATTACGTGGTAAGGTAATTAATACAGAGAAAGCACGTCTAGAAGATATTTTTAAAAATGAAGAAATTAATACA
       1391       1401       1411       1421       1431       1441       1451       1461

       I   I   H   T   I   G   A   S   V   G   T   D   F   K   I   E   D   S   N   Y   N   R   V   I   I
       ATTATCCACACAATCGGGGCAGGCGTTGGTACTGACTTTAAAATTGAAGATAGTAATTATAATCGTGTAATTATT
       1466       1476       1486       1496       1506       1516       1526       1536

       M   T   D   A   D   T   D   G   A   H   I   Q   V   L   L   L   T   F   F   F   K   Y   M   Y   F
       ATGACTGATGCTGATATTGATGGTGCGCATATTCAAGTGCTATTGTTAACATTTTTTTTCAAATATATGAAACCG
       1541       1551       1561       1571       1581       1591       1601       1611

       L   V   Q   A   G   R   V   F   I   A   L   P   F   L   Y   K   L   E   K   G   K   G   K   T   K
       CTTGTTCAAGCAGGTCGTGTATTTATTGCTTTACCTCCACTTTATAAATTGGAAAAAGGTAAAGGCAAAACAAAG
       1616       1626       1636       1646       1656       1666       1676       1686
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    K  V  E  Y  A  K  T  C  E  E  L  K  K  L  C  K  E  L  S  K  G  F  T  L  Q
    CGAGTTGAATATGCTTGGACAGATGAAGAGCTTAATAAATTGCAAAAAGAACTTCGTAAAGGCTTCACGTTACAA
    1691      1701      1711      1721      1731      1741      1751      1761

    R  Y  K  G  L  G  E  M  N  F  E  Q  L  K  E  T  T  M  K  F  E  T  R  T  L
    CGTTACAAAGGTTTGGGTGAAATGAACCCTGAACAATTATGGGAAACGACGATGAACCCAGAAACACGAACTTTA
    1766      1776      1786      1796      1806      1816      1826      1836

    I  R  V  Q  V  E  D  E  V  R  S  S  K  R  V  T  T  L  M  G  D  K  V  Q  F
    ATTCGTGTACAAGTTGAAGATGAAGTGCGTTCATCTAAACGTGTAACAACATTAATGGGTGACAAAGTACAACCT
    1841      1851      1861      1871      1881      1891      1901      1911

    R  R  E  W  I  E  K  H  V  E  F  G  M  Q  E  D  C  S  I  L  D  N  S  E  V
    AGACGTGAATGGATTGAAAAGCATGTTGAGTTTGGTATGCAAGAGGACCAAAGTATTTTAGATAATTCTGAAGTA
    1916      1926      1936      1946      1956      1966      1976      1986

    Q  V  L  E  N  D  Q  F  D  E  E  E  I  ***
    CAAGTGCTTGAAAATGATCAATTTGATGAGGAGGAAATCTAG
    1991      2001      2011      2021
```

(5)   INFORMATION FOR SEQ ID NO: 4:


    (i)    SEQUENCE CHARACTERISTICS:

           (A)   LENGTH: 30 bases

           (B)   TYPE: nucleic acid

           (C)   STRANDEDNESS: single

           (D)   TOPOLOGY: linear


    (ii)   MOLECULE TYPE: cDNA


    (iii)  HYPOTHETICAL: NO


    (iii)  ANTISENSE: NO


    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 4:


           GCGCGAATTC GATGGWYTWA AACCWGTWCA


(6)   INFORMATION FOR SEQ ID NO: 5:

       (i)    SEQUENCE CHARACTERISTICS:

              (A)   LENGTH: 31 bases

              (B)   TYPE: nucleic acid

              (C)   STRANDEDNESS: single

5             (D)   TOPOLOGY: linear


       (ii)   MOLECULE TYPE: cDNA


       (iii)  HYPOTHETICAL: NO


       (iii)  ANTISENSE: YES


       (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 5:


10            CGCGAAGCTT TTCWGTATAW CKCATWGCWG C


(7)    INFORMATION FOR SEQ ID NO: 6:


       (i)    SEQUENCE CHARACTERISTICS:

              (A)   LENGTH: 29 bases

              (B)   TYPE: nucleic acid

              (C)   STRANDEDNESS: single

15            (D)   TOPOLOGY: linear


       (ii)   MOLECULE TYPE: cDNA


       (iii)  HYPOTHETICAL: NO

(iii) ANTISENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCGCGAATTC TWCATGCWGG WGGWAAATT

(8) INFORMATION FOR SEQ ID NO: 7:

5           (i)   SEQUENCE CHARACTERISTICS:

                  (A)  LENGTH: 31 base pairs

                  (B)  TYPE: nucleic acid

                  (C)  STRANDEDNESS: single

                  (D)  TOPOLOGY: linear

10          (ii)  MOLECULE TYPE: cDNA

            (iii) HYPOTHETICAL: NO

            (iii) ANTISENSE: NO

            (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 7:

                  CGCGAAGCTT WCCWCCWGCW GAATCWCCTT C

15    (9)   INFORMATION FOR SEQ ID NO: 8:

            (i)   SEQUENCE CHARACTERISTICS:

                  (A)  LENGTH: 7 amino acids

(B)  TYPE: amino acid

(D)  TOPOLOGY: linear


(ii)  MOLECULE TYPE: protein


(iii)  HYPOTHETICAL: NO


5        (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 8:


            Ala Ala Met Arg Tyr Thr Glu
                            5



(10) INFORMATION FOR SEQ ID NO: 9:


        (i)    SEQUENCE CHARACTERISTICS:
10             (A)  LENGTH: 7 amino acids
               (B)  TYPE: amino acid
               (D)  TOPOLOGY: linear


    (ii)  MOLECULE TYPE: protein


    (iii)  HYPOTHETICAL: NO


15    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 9:


            Tyr His Pro His Gly Asp S r
                            5

(11) INFORMATION FOR SEQ ID NO: 10:

       (i)      SEQUENCE CHARACTERISTICS:

              (A)   LENGTH: 29 bases

              (B)   TYPE: nucleic acid

5              (C)   STRANDEDNESS: single

              (D)   TOPOLOGY: linear

       (ii)    MOLECULE TYPE: cDNA

       (iii)   HYPOTHETICAL: NO

       (iii)   ANTISENSE: NO

10         (xi)    SEQUENCE DESCRIPTION: SEQ ID NO: 10:

              GGCGGATCCC ATATGGCTGA ATTACCTCA

(12) INFORMATION FOR SEQ ID NO: 11:

       (i)      SEQUENCE CHARACTERISTICS:

              (A)   LENGTH: 29 bases

15            (B)   TYPE: nucleic acid

              (C)   STRANDEDNESS: single

              (D)   TOPOLOGY: lin ar

       (ii)    MOLECULE TYPE: cDNA

(iii)  HYPOTHETICAL: NO

(iii)  ANTISENSE: NO

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCGGAATTC GACGGCTCTC TTTCATTAC

5    (13) INFORMATION FOR SEQ ID NO: 12:

(i)    SEQUENCE CHARACTERISTICS:
       (A)  LENGTH: 35 bases
       (B)  TYPE: nucleic acid
       (C)  STRANDEDNESS: single
10                (D)  TOPOLOGY: linear

(ii)   MOLECULE TYPE: cDNA

(iii)  HYPOTHETICAL: NO

(iii)  ANTISENSE: NO

(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 12:

15          GGCCGGATCC CATATGAGTG AAATAATTCA AGATT

(14) INFORMATION FOR SEQ ID NO: 13:

(i)    SEQUENCE CHARACTERISTICS:

    (A)   LENGTH: 32 bases

    (B)   TYPE: nucleic acid

    (C)   STRANDEDNESS: single

5        (D)   TOPOLOGY: linear


(ii)   MOLECULE TYPE: cDNA


(iii)  HYPOTHETICAL: NO


(iii)  ANTISENSE: YES


(xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 13:


10        GGCCGAATTC TAATAATTAA CTGTTTACGT CC


(15) INFORMATION FOR SEQ ID NO: 14:


(i)    SEQUENCE CHARACTERISTICS:

    (A)   LENGTH: 32 bases

    (B)   TYPE: nucleic acid

15      (C)   STRANDEDNESS: single

    (D)   TOPOLOGY: linear


(ii)   MOLECULE TYPE: cDNA


(iii)  HYPOTHETICAL: NO

(iii)   ANTISENSE: YES


(xi)    SEQUENCE DESCRIPTION: SEQ ID NO: 14:


     GGCCGAGCTC CAATTCTTCT TTTATGACAT TC